



SEQUENCE LISTING

<110> Russo, Giandomenico
Croce, Carlo M.

<120> TCL-1 GENE AND PROTEIN AND RELATED
METHODS AND COMPOSITIONS

<130> 3589.1017-001

<140> 09/441,242

<141> 1999-11-16

<150> 08/330,272

<151> 1994-10-27

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1324

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence of TCL-1

<221> CDS

<222> (49)...(387)

<400> 1

cttgagaggc tctggctctt gcttcttagg cggcccgagg acgccatg gcc gag tgc 57
Ala Glu Cys
1

cgg aca ctc ggg gag gca gtc acc gac cac ccg gac cgc ctg tgg gcc 105
Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala
5 10 15

tgg gag aag ttc gtg tat ttg gac gag aag cag cac gcc tgg ctg ccc 153
Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro
20 25 30 35

tta acc atc gag ata aag gat agg tta cag tta cgg gtg ctc ttg cgt 201
Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg
40 45 50

cgg gaa gac gtc gtc ctg ggg agg cct atg acc ccc acc cag ata ggc 249
Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly
55 60 65

cca agc ctg ctg cct atc atg tgg cag ctc tac cct gat gga cga tac 297
Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr
70 75 80

cga tcc tca gac tcc agt ttc tgg cgc tta gtg tac cac atc aag att 345
Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile
85 90 95

gac ggc gtg gag gac atg ctt ctc gag ctg ctg cca gat gac 387
Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp Asp
100 105 110

tgatgtatgg	tcttggcagc	acctgtctcc	tttcacccca	gggctgagc	ctggccagcc	447
tacaatgggg	atgttggtgt	tctgttcacc	ttcgtttact	atgcctgtgt	cttctccacc	507
acgctggggg	ctgggaggaa	tggacagaca	gaggatgagc	tctacccagg	gcctgcagga	567
cctgcctgta	gccactctg	ctcgccttag	cactaccact	cctgccaaag	aggattccat	627
ttggcagagc	ttcttccagg	tgcccagcta	tacctgtgcc	tcggcttttc	tcagctggat	687
gatgggtcttc	agcctctttc	tgtcccttct	gtccctcac	gcactagtat	ttcatgttgc	747
acacccactc	agctccgtga	acttgtgaga	acacagccga	ttcacttgag	caggacctct	807
gaacccctgg	accagtggtc	tcacatgggtg	ctacgcctgc	atgtaaacac	gcctgcaaac	867
gctgcctgcc	ggtaaacacg	cctgcaaacg	ctgcctgccc	gtaaacacgc	ctgcaaacgc	927
tgcttgccca	cacaggttca	cgtgcagctc	aaggaaaggc	ctgaaaggag	cccttatctg	987
tgctcaggac	tcagaagcct	ctgggtcagt	ggtcacatc	ccgggacgca	gcaggaggcc	1047
aggccggcga	gccctgtgga	tgagccctca	gaacccttgg	cttgcccacg	tggaaaaggg	1107
atagaggttg	ggtttccccc	ctttatagat	ggtcacgcac	ctgggtgtta	caaagttgta	1167
tgtggcatga	atactttttg	taagtattga	ttaagtcaa	gatagtttat	ctaacttcgt	1227
gcgcaatcag	cttctatcct	tgacttagat	tctggtggag	agaagtgaga	ataggcagcc	1287
cccaaataaa	aaatatccat	qgaaaaaaaa	aaaaaaa			1324

<210> 2

<211> 113

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> cDNA sequence of TCL-1

<400> 2

[illegible] $\langle 210 \rangle$ 3

<211> 560

<212> DNA

<213> Artificial Sequence

<220>

<223> genomic sequence of TCL-1

<400> 3

```

gtcgactgtg agttcccagc agaggcccag agtccccggtc cggcagccga gggaagcggg 60
ggggtcttcc agaagaagaa agggccaagg tcaccccggg gcctctccag cagcagcaga 120
gggcggcggg cgggtgtcgt gctggccggg gcctcgagga aggcgcgggc cagctggggc 180
cgggtctgcg ttcccaggag ctgccaccgt tccagggagc aagtcaggcc gggacgttag 240
cgctgcgcgc ggaccctcac ttgccaccaa ggaccccaca aaccccgcgc catccttagc 300
gcctgcgcgc gaccctcact tgccaccaag acccccacaa accccgcgcc atcctgcctt 360
acgccccgcc ccaaggtcgt tctcccgacc cgggggtccc cccaagacc gtcctcccgc 420
ccgcgcgctt ggtggcggcc gcatgctgcc cggatataaa gggtcggccc cacatcccag 480
ggaccagcga gcggccttga gaggtctctg ctcttgcttc ttaggcggcc cgaggacgcc 540
atggccgagt gcccgacact                    560

```

<210> 4

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> MTCPl protein

<221> SITE

<222> 108

<223> Xaa = any amino acid

<221> VARIANT

<222> 108

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 108

<223> Xaa = Any Amino Acid

<400> 4

```

Met Ala Gly Glu Asp Val Gly Ala Pro Pro Asp His Leu Trp Val His
 1           5           10           15
Gln Glu Gly Ile Tyr Arg Asp Glu Tyr Gln Arg Thr Trp Val Ala Val
      20           25           30
Val Glu Glu Glu Thr Ser Phe Leu Arg Ala Arg Val Gln Gln Ile Gln
      35           40           45
Val Pro Leu Gly Asp Ala Ala Arg Pro Ser His Leu Leu Thr Ser Gln
      50           55           60
Leu Pro Leu Met Trp Gln Leu Tyr Pro Glu Glu Arg Tyr Met Asp Asn
      65           70           75           80
Asn Ser Arg Leu Trp Gln Ile Gln His His Leu Met Val Arg Gly Val
      85           90           95
Gln Glu Leu Leu Leu Lys Leu Leu Pro Asp Asp Xaa
      100           105

```

<210> 5

<211> 4922

<212> DNA

<213> Artificial Sequence

<220>

<223> genomic DNA of TCL-1

<221> misc_feature

<222> (1)...(4922)

<223> n = A,T,C or G

<400> 5

```

gtcgacttgt gakttyccmag magaggccca gaagtcccg tccggcaaag cggaggggaa 60
gcgggggggg tcttccaaga agaagaaagg gcccaaggtt caacccccgg tgccttctcc 120
agcagcaagc aagagggcgg cgggtcgggt gtcgctgctg gccggggccc tccgaggaaa 180
ggcgcggrcc agctggggcc gggctctgctg tcccaggagc tgccaccgtt ccaggagaca 240
agtacggccg ggacgttagc gcctgcgcgg gacctcact tgccaccaag rmccccacaa 300
accccgcccc atcctgyctt acgccccgcc ccaaggtcgg ttctccccga cccgggggtc 360
ccgcccccaa ggncgctect ccccgcccc gccgsttggg ggcgggcgca tgcctggcgc 420
atataaaggg tcggccccac atcccaggga ccagcgagcg gccttgagag gctctggctc 480
ttgcttctta ggcgccccga ggacgccatg gccgagtgcc cgacactcgg ggaggcagtc 540
accgaccacc cggaccgcct gtgggcctgg gagaagttcg tgtatttggg cgagaagcag 600
macgcctgcc tgcccttaac catcgaggta caaccacct tggagcggat ggcgargcag 660
caggggcasc ccctgggagc ttgggatncc ctaggaaggg cgaggactca aggagcactc 720
actatggggc agggaggatc ccccacagat kaagccactt ttggagccgg sctctkgagg 780
gatgaatagg agttcctcca ggcaggggaa aagggtgagg aaaccccaaa ggaatgtcgg 840
tcaaaggggt ggacccagtg cctgtggagt gtgactataa tgttgactac agcaggcatt 900
ttctgggctt cggggtccta atccttaaaa atgggtatct ctaagtgact catccatatg 960
gccgattatc ggaatcatct caggtgggtc ccagaaatct gtatttttaa aaagaacccw 1020
cmacagttta ggggtccaacc caggcataac caaaacactg gcctaagagt tgtgaagtat 1080
tttcccacct accctctggg ctttatttaa gamaaccaa ttaacaagt gatgtcgtag 1140
tataagcgcc ggtantkgaa ycaatattga cttttttaat gtgtgatgcc ttaagatggg 1200
tccttaatcc atgttaagnt tttgttaaag aaatagataa gtcttttaca agtatttgga 1260
tttactcaat gaaaaagagt canaaaatgt tcaaactctc tccaaacata cactgaagaa 1320
agcataaaaa ttannaaata tattagaaca cgtatgtcca gtagcaawca maaattattg 1380
agtgttgayt gtgtctctac agatgggaaa ctgaggcaca cmaaagtac atttgtccga 1440
ggtaagattg ctagtaggta atgggggttg aattctaggc tcttaaccac cacaaaatct 1500
gcatttttat tggcatttca atttttttaa tatgttttta ctttaaaaat caagttaaat 1560
acttactttt ttaaaatcaa aatttgaaga aataatttga agattcagtg gatttctttt 1620
tttaaactct tgagaaatct ctccctyca acgtgacacc maaaccmgcg aaccagacag 1680
tttttcataa aatcatgaaa catgcyccmc maaaaataac ccactascaa actgtgggac 1740
agattttgcc tcacatcatt gaaaaggcca gcawtctttt tctctctttc tttctttgkt 1800
gttttttttt tttcctgtag awacagggtc tcgctctgtg acccaggctg gtctyaaact 1860
cctggcctca agcgatcctc ctgcctctgc cttccaaagc actggaatta caagtgtgag 1920
ccgctgcaac ccgccagaaa aaagtgtgcc tttcatggcc ctgtctgggt ggctagacac 1980
gtgtgtgtgc tgggtggtcct ggcccagcca gagttccctg agaggagcat gcatggccta 2040
aggaagtgag cttcagggaa cagtgatgac catcatttca cactcggacc ccctgccmaa 2100
gatgggtgga tgsctgscag ggagggattc cggtkttcct gcgcctggag aanccctgcc 2160
aagcggaacc tgaaagtatn ccctgtcctt ttcttctcct nagataaagg ataggttaca 2220
gttnnggggtg ctcttgctgc gggaagacgt cgtcctgggg aggcctatga cccccaccna 2280
gataggccca agcctgctgc ctatcatgtg gcagctctac cctgatggac gataccgatc 2340
ctcagactcc agtttctggc gcttagtgta ccacatcaag gtgagtgtct ttctcccaga 2400
ggtccatccc ktgatcttgg gtttccctc cymatgtct gsccttagtg gtttaycttc 2460
ccyccatccc agtssgcaaa agcattwaaa aratggggga nrtrwacmas tgcagatttc 2520
tanaggactt taccagagag aaganagatc ctntgaggtc tctaanagaa ccctacctcc 2580
acttctctcc anccaccanc taaccgcagg aagacatctc tgggtggggmm kcacaggctg 2640
aaggctgggt ggaggaggr caktctccaa gasccctga aatcctcaca cctgggttcc 2700
tacctgctgt ttccagctag gggaagscsc aggagtgagg aatggaggga gtggagggct 2760
ctggccgatc aatgccttct ctctctctct gcctctcaga ttgacggcgt ggaggacatg 2820
cttctcgagc tgctgccaga tgactgatgt atgggtgagct ccactggagc ctgacccctc 2880
ttagtccaca gtggctgtat cagaaagaaa gaccaccctt tctccatgaa ggcagtgtca 2940

```

```

accctcccc gactgctgcc atctgagggg ccctagggat gggagaggct tcctggaggc 3000
actcatgtct cccttaccac ttcgggagcc aagggtttg gtaggcagcc ccctttatcg 3060
cagctgctca tatctataaa gtacttcaca agtttcagct ggcactttca ttttaccatt 3120
gctttttttt tctttgggag atgagtctgg ctctgtggcc caggctagag tgtagtgggt 3180
gcaatctcag ctactgaaa gctctgcctc ccgggttcac accattctcc tgcctcagcc 3240
ctcggagtag ctgggactac aggcgcccgc caccacacct ggctaatttt tttttttttw 3300
ttwtwttttt tagtagagmc ggggtttcac cgtgttagcc aggatggtct cgatecctg 3360
acctcatgat ctgcccgcct cggcctcca aagtgtggg attacaggca tgagccacca 3420
cgtccggcct taccattgct ttattaaata agcactgggt cttgattata tcagctgagc 3480
cagatattag atacgctatt gagttttgrg gaaataagag taccaaaact cagaaatgag 3540
ttgaagtata gtgacatctt cagattacag acccaggtgt cagaatttgc cttgggtcag 3600
aaggcctctg ggggccatcc ctgaccacta ggcttcccac ttagacctgc tccagcagca 3660
ccaccctcg scactgcctg gtcctttcct tcacccttga ttctgtcttc ttttgcctt 3720
ctccaggtct tgggagcacc tgtctccttt caccacaggg cctgagcctg gccagcctac 3780
aatggggatg ttgtgtttct gttcaccttc gtttactatg bctgtgtctt ctccaccacg 3840
ctggggtctg ggaggaatgg acagacagag gatgagctct acccrgggcc tgsaggacct 3900
gtcctgtagm ccactctgct cgccttaga cctacsactc cwrccgasga ggatnccant 3960
tggaagagct tcttnnagggt gncnaanaan anctgtgcgt nggcttttct cagctggatg 4020
atggtcntna gcctctttct gtccttctctg tccctcacag cactagtatt tnatgttgca 4080
caccactca gctccgtgaa tttgtgagaa cacaaccgat tcacctgagc aggacctctg 4140
aaaccctgga ccagtggctc cacatgggtc tacgcctgca tgtaaacacg cctncaaacg 4200
ctgcctgck gtraaacacgm sksyrmacag stgmswrcc gtaaacacgc ctgcaaacgc 4260
tgctcaggac tcagaagcct ctgggtcagt ggtccacatc ccgggacgca gnaggaggcc 4380
aggccggcga gccctgtgga tgagccctca gaacccttgg gttgccacg tggaaaagg 4440
atagaggttg ggtttcccc cttttataga tggtcacgca cctgggtgtt acaaagtgt 4500
atgtggcatg aatacttgnt gtnatgattg attaaatgca agatagtta tctaacttcg 4560
tgcggaatca gcttctatcc ttgncttaga ttctgggtga gagaagtgan aataggcagn 4620
cccanataa anaatattca ngggatttat tttattnttc cttttggng atnngggact 4680
acattntn nccccgtnta atccaatgnt taaancccca gtgttcttgg aggnctacg 4740
tcgaanacca ttgngtang caacctcaaa atttttnngt tgnnaattnc cngttttcca 4800
gagnccccc cntnctccat cttntectn gccnccctn ncctccnca ntcccnangt 4860
tnccctcgnc cccagtcagt tctttctccn nctttanccg ntatntcac cagnttctt 4920
ct

```

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> p9A primer

<400> 6

tgctgccaga tgactgatgt

20

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Rev III primer

<400> 7

caaatggaat cctccttggc

20

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Daudi unil- primer

<400> 8
aggcctatga cccccacc 18

<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Daudi rev2 primer

<400> 9
cattcctccc agacccca 18

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> A1 primer

<400> 10
tcatcaccat tggcaatgag 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> A2 primer

<400> 11
cagtgtgttg gcgtacaggt 20

<210> 12
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> TCL-1 protein

<221> SITE
<222> 113
<223> Xaa = any amino acid

<221> VARIANT

<222> 113

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 113

<223> Xaa = Any Amino Acid

<400> 12

Met	Ala	Glu	Cys	Pro	Thr	Leu	Gly	Glu	Ala	Val	Thr	Asp	His	Pro	Asp
1				5					10					15	
Arg	Leu	Trp	Ala	Trp	Glu	Lys	Val	Tyr	Leu	Asp	Glu	Lys	Gln	His	Ala
			20					25					30		
Trp	Leu	Pro	Leu	Thr	Ile	Glu	Ile	Lys	Asp	Arg	Leu	Gln	Leu	Arg	Val
		35				40						45			
Leu	Leu	Arg	Arg	Glu	Asp	Val	Val	Leu	Arg	Ser	Met	Thr	Pro	Thr	Gln
	50					55					60				
Ile	Gly	Pro	Ser	Leu	Leu	Pro	Ile	Met	Trp	Gln	Leu	Tyr	Pro	Asp	Gly
65					70					75					80
Arg	Tyr	Arg	Ser	Ser	Asp	Ser	Ser	Phe	Trp	Arg	Leu	Val	Tyr	His	Ile
				85					90					95	
Lys	Ile	Asp	Gly	Val	Glu	Asp	Met	Leu	Leu	Glu	Leu	Leu	Pro	Asp	Asp
			100					105						110	

Xaa